

## THAT WHICH IS CLAIMED:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- 5           a) an amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, or 19;
- 10          b) an amino acid sequence having at least 70% identity to at least one of the amino acid sequences set forth in SEQ ID NO: 6, 8, 12, 14, or 19, wherein said polypeptide comprises thioredoxin activity;
- 15          c) an amino acid sequence having at least 75% identity to at least one of the amino acid sequences set forth in SEQ ID NO: 2, 4, or 10, wherein said polypeptide comprises thioredoxin activity; and
- d) an amino acid sequence having at least 95% identity to at least one of the amino acid sequences set forth in SEQ ID NO: 16, wherein said polypeptide comprises thioredoxin activity.

2. An isolated polypeptide comprising the amino acid sequence selected from the group consisting of:

- 20          a) an amino acid sequence set forth in SEQ ID NO: 21, 23, or 25;
- b) an amino acid sequence having at least 80% identity to at least one of the amino acid sequences set forth in SEQ ID NO: 21 or 25, wherein said polypeptide comprises thioredoxin reductase activity; and
- 25          c) an amino acid sequence having at least 85% identity to at least one of the amino acid sequences set forth in SEQ ID NO: 23, wherein said polypeptide comprises thioredoxin reductase activity.

3. An isolated nucleotide molecule comprising a nucleotide sequence selected from the group consisting of:

- 30          a) a nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 18;

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- 5                   b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, or 19;
- 10                 c) an nucleotide sequence having at least 95% sequence identity to the coding sequence of at least one of the nucleotide sequences set forth in a), wherein said nucleotide sequence encodes a polypeptide comprising thioredoxin activity;
- 15                 d) a nucleotide sequence that hybridizes under stringent conditions to at least one of the nucleotide sequence set forth in a), wherein said nucleotide sequence encodes a polypeptide comprising thioredoxin activity; and
- 20                 e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d), wherein said nucleotide sequence is capable of antisense suppression of thioredoxin expression in a cell.
- 25                 4. An isolated nucleotide molecule comprising a nucleotide sequence selected from the group consisting of:
- 30                 a) a nucleotide sequence set forth in SEQ ID NO: 20, 22, or 24;
- 35                 b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 21, 23, or 25;
- 40                 c) an nucleotide sequence having at least 95% sequence identity to the coding sequence of at least one of the nucleotide sequences set forth in a);
- 45                 d) a nucleotide sequence that hybridizes under stringent conditions to at least one of the nucleotide sequence set forth in a); and
- 50                 e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d), wherein said nucleotide sequence is capable of antisense suppression of thioredoxin reductase expression in a cell.
- 55                 5. An expression cassette comprising the nucleotide molecule of claim 3, wherein said nucleotide sequence is operably linked to a promoter.

6. A non-human host cell transformed with the expression cassette of  
claim 5.

5 7. The host cell of claim 6, wherein said host cell is a plant cell.

8. An expression cassette comprising the nucleotide molecule of claim 4,  
wherein said nucleotide sequence is operably linked to a promoter.

10 9. A non-human host cell transformed with the expression cassette of  
claim 8.

10. The host cell of claim 9, wherein said host cell is a plant cell.

15 11. A transformed plant comprising in its genome at least one stably  
incorporated nucleotide construct comprising at least one nucleotide sequence, said  
nucleotide sequence selected from the group consisting of:

- a) a nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15,  
17, or 18;
- b) a nucleotide sequence encoding the amino acid sequence set forth in  
SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, or 19;
- c) a nucleotide sequence set forth in SEQ ID NO: 20, 22, or 24;
- d) a nucleotide sequence encoding the amino acid sequence set forth in  
SEQ ID NO: 21, 23, or 25;
- e) an nucleotide sequence having at least 95% sequence identity to the  
coding sequence of at least one of the nucleotide sequences set forth in  
a) or c), wherein said nucleotide sequence encodes a polypeptide  
comprising thioredoxin activity or thioredoxin reductase activity;
- f) a nucleotide sequence that hybridizes under stringent conditions to at  
least one of the nucleotide sequence set forth in a) or c), wherein said

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nucleotide sequence encodes a polypeptide comprising thioredoxin activity or thioredoxin reductase activity; and  
5           g) a nucleotide sequence that is complementary to the nucleotide sequence of a)-f), wherein said nucleotide sequence is capable of antisense suppression of thioredoxin expression or thioredoxin reductase expression in a cell.

10           12. The plant of claim 11, wherein said nucleotide construct further comprises

an operably linked promoter that drives expression in a plant cell.

15           13. The plant of claim 12, wherein said promoter is operably linked to said

nucleotide sequence for the production of antisense transcripts.

15           14. The plant of claim 12, wherein said promoter is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.

20           15. The plant of claim 12, wherein said plant comprises in its genome a first nucleotide construct comprising the nucleotide sequence of c), d), or e), wherein said nucleotide sequence encodes a polypeptide comprising thioredoxin reductase activity.

25           16. The plant of claim 15, wherein said plant comprises in its genome a second nucleotide construct comprising the nucleotide sequence of a), b), or e), wherein said nucleotide sequence encodes a polypeptide comprising thioredoxin activity.

17. The plant of claim 11, wherein said plant is a monocot.

30           18. The plant of claim 17, wherein said monocot is selected from the group consisting of maize, wheat, rice, sorghum, barley, millet and rye.

19. The plant of claim 11, wherein said plant is a dicot.

20. The plant of claim 19, wherein said dicot is selected from the group consisting of soybean, *Brassica sp.*, alfalfa, safflower, sunflower, cotton, peanut and potato.
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21. Transformed seed of the plant of claim 11.
22. A method for altering the disulfide status of storage proteins in a plant or part thereof, said method comprising transforming said plant with a nucleotide construct
- 10 comprising a nucleotide sequence encoding NADPH-thioredoxin reductase, wherein said nucleotide sequence is selected from the group consisting of:
- a) a nucleotide sequence set forth in SEQ ID NO: 20, 22, or 24;
- b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 21, 23, or 25;
- 15 c) an nucleotide sequence having at least 95% sequence identity to the coding sequence of at least one of the nucleotide sequences set forth in a);
- d) a nucleotide sequence that hybridizes under stringent conditions to at least one of the nucleotide sequence set forth in a); and
- 20 e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d);
- wherein said disulfide status of said storage proteins is altered in said plant or part thereof.
- 25 23. The method of claim 22 further comprising transforming said plant with an additional nucleotide construct comprising a nucleotide sequence encoding thioredoxin *h*, wherein said nucleotide sequence is selected from the group consisting of:
- a) a nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 18;
- 30 b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, or 19,

- c) an nucleotide sequence having at least 95% sequence identity to the coding sequence of at least one of the nucleotide sequences set forth in a);
  - d) a nucleotide sequence that hybridizes under stringent conditions to at least one of the nucleotide sequence set forth in a); and
  - e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d).
24. The method of claim 22, wherein said part is seed or grain.
25. The method of claim 22, wherein at least one of said nucleotide constructs further comprises an operably linked promoter that drives expression in a plant cell.
26. The method of claim 25, wherein said promoter is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.
27. The method of claim 25, wherein said promoter is operably linked to said nucleotide sequence for the production of antisense transcripts.
28. The method of claim 22, further comprising chimeroplasty.
29. A method for improving the digestibility of grain, said method comprising transforming a plant with a nucleotide construct comprising a promoter that drives expression in a plant cell operably linked to a nucleotide sequence encoding NADPH-thioredoxin reductase, wherein said nucleotide sequence is selected from the group consisting of:
  - a) a nucleotide sequence set forth in SEQ ID NO: 20, 22, or 24;
  - b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 21, 23, or 25;

- c) an nucleotide sequence having at least 95% sequence identity to the coding sequence of at least one of the nucleotide sequences set forth in a);
- d) a nucleotide sequence that hybridizes under stringent conditions to at least one of the nucleotide sequence set forth in a); and
- e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d);

wherein said digestibility of said grain is increased when consumed by an animal.

10        30. The method of claim 29 further comprising transforming said plant with a nucleotide construct comprising a promoter that drives expression in a plant cell operably linked to a nucleotide sequence encoding thioredoxin *h*, wherein said nucleotide sequence is selected from the group consisting of:

- a) a nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, or 18;
  - b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, or 19,
  - c) an nucleotide sequence having at least 95% sequence identity to the coding sequence of at least one of the nucleotide sequences set forth in a);
  - d) a nucleotide sequence that hybridizes under stringent conditions to at least one of the nucleotide sequence set forth in a); and
  - e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d).

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31. The method of claim 29, wherein at least one of said promoters is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.

32. The method of claim 29, wherein said animal is selected from the group consisting of a human, a chicken, a cow, a pig, a turkey, a goat, a sheep, a dog, a cat and a fish.

5 33. The method of claim 29, wherein the grain is a mature maize kernel.

34. The method of claim 29, wherein the grain is a kernel that is part of whole plant corn harvested for silage.

10 35. A method for altering grain hardness, said method comprising transforming a plant with a nucleotide construct comprising a nucleotide sequence encoding NADPH-thioredoxin reductase, wherein said nucleotide sequence is selected from the group consisting of:

- a) a nucleotide sequence set forth in SEQ ID NO: 20, 22, or 24;
- 15 b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 21, 23, or 25;
- c) an nucleotide sequence having at least 95% sequence identity to the coding sequence of at least one of the nucleotide sequences set forth in a);
- 20 d) a nucleotide sequence that hybridizes under stringent conditions to at least one of the nucleotide sequence set forth in a); and
- e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d);

wherein the hardness of said grain is increased or decreased.

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36. The method of claim 35 further comprising transforming said plant with an additional nucleotide construct comprising a nucleotide sequence encoding thioredoxin *h*, wherein said nucleotide sequence is selected from the group consisting of:

- a) a nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 30 17, or 18;

- b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, or 19,
  - c) an nucleotide sequence having at least 95% sequence identity to the coding sequence of at least one of the nucleotide sequences set forth in a);
  - d) a nucleotide sequence that hybridizes under stringent conditions to at least one of the nucleotide sequence set forth in a); and
  - e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d).

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37. The method of claim 35, wherein at least one of said nucleotide constructs further comprises an operably linked promoter that drives expression in a plant cell.

38. The method of claim 37, wherein said promoter is selected from the group  
15 consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and  
developmentally regulated promoters.

39. The method of claim 37, wherein said promoter is operably linked to said nucleotide sequence for the production of antisense transcripts.

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40. The method of claim 35 further comprising chimeroplasty.

41. The method of claim 35, wherein said grain hardness is increased and the digestibility of said grain is decreased when consumed by an animal.

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42. The method of claim 35, wherein said grain hardness is increased and the energy availability from said grain when consumed by an animal is decreased.

43. The method of claim 42, wherein said animal is a human, dog or cat.

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44. The method of claim 41, wherein the animal is a ruminant and the protein degradability in the rumen of the animal is decreased.

45. A method for improving grain for processing, said method comprising  
5 transforming a plant with a nucleotide construct comprising a promoter that drives  
expression in a plant cell operably linked to a nucleotide sequence encoding NADPH-thioredoxin reductase, wherein said nucleotide sequence is selected from the group  
thioredoxin reductase, wherein said nucleotide sequence is selected from the group  
consisting of:

- a) a nucleotide sequence set forth in SEQ ID NO: 20, 22, or 24;
- b) a nucleotide sequence encoding the amino acid sequence set forth in  
SEQ ID NO: 21, 23, or 25;
- c) an nucleotide sequence having at least 95% sequence identity to the  
coding sequence of at least one of the nucleotide sequences set forth in  
a);
- d) a nucleotide sequence that hybridizes under stringent conditions to at  
least one of the nucleotide sequence set forth in a); and
- e) a nucleotide sequence that is complementary to the nucleotide  
sequence of a), b), c), or d);

wherein said grain is improved for processing.

46. The method of claim 45 further comprising transforming said plant with a nucleotide construct comprising a promoter that drives expression in a plant cell operably linked to a nucleotide sequence encoding thioredoxin *h*, wherein said nucleotide sequence is selected from the group consisting of:

25           a) a nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15,  
               17, or 18;  
          b) a nucleotide sequence encoding the amino acid sequence set forth in  
               SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, or 19,  
          c) an nucleotide sequence having at least 95% sequence identity to the  
               coding sequence of at least one of the nucleotide sequences set forth in  
               a);  
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- d) a nucleotide sequence that hybridizes under stringent conditions to at least one of the nucleotide sequence set forth in a); and
- e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d).

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47. The method of claim 45, wherein at least one of said promoters is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.

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48. The method of claim 45, wherein the processing is wet milling and the improvement is increased starch extractability, decreased need for chemical reducing agents, or improved digestibility of wet milling by-products.

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49. The method of claim 45, wherein the processing is grinding and the

improvement is a higher degree of particle size reduction or energy savings.

50. The method of claim 45, wherein the processing is steam flaking and the improvement is a larger improvement in digestibility enhancement by steam flaking or energy savings.

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51. The method of claim 45, wherein the processing is dry grind ethanol production and the improvement is increased fermentable starch or increased digestibility of fermentation by-products.

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52. A method for altering the disulfide status of storage proteins in a plant or part thereof, said method comprising transforming said plant with a nucleotide construct comprising a nucleotide sequence encoding NADPH-thioredoxin reductase, wherein said disulfide status of said storage proteins is altered in said plant or part thereof.

53. The method of claim 52 further comprising transforming said plant with an additional nucleotide construct comprising a nucleotide sequence encoding thioredoxin *h*.

5 54. The method of claim 52, wherein said part is seed or grain.

55. The method of claim 52, wherein at least one of said nucleotide constructs further comprises an operably linked promoter that drives expression in a plant cell.

10 56. The method of claim 52, wherein said promoter is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.

15 57. The method of claim 56, wherein said promoter is operably linked to said nucleotide sequence for the production of antisense transcripts.

58. The method of claim 52, further comprising chimeraplasty.

59. The method of claim 54, wherein the digestibility of said grain is increased when consumed by an animal.

20 60. The method of claim 54, wherein the hardness of said grain is increased or decreased.

25 61. The method of claim 54, wherein said grain is improved for processing.